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# 9

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/673,166

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences  
(OLD RULES) Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences  
(NEW RULES) Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>  
Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is **not** used to represent any value not specifically a nucleotide.

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,166

DATE: 08/19/2002

TIME: 12:54:26

Input Set : A:\102.174.txt

Output Set: N:\CRF3\08192002\I673166.raw

3 <110> APPLICANT: Le Gal, Frederique Anne  
 4 Guillet, Jean Gerard  
 5 Gahery-Segard, Hanne  
 6 Gras-Masse, Helene  
 7 Melnyk, Oleg  
 8 Tartar, Andre  
 10 <120> TITLE OF INVENTION: LIPOPEPTIDES INDUCING T LYMPHOCYTIC CYTOTOXICITY  
 11 BEARING AT LEAST ONE AUXILIARY T EPITOPE, AND USES FOR  
 12 VACCINATION  
 14 <130> FILE REFERENCE: 102.174  
 16 <140> CURRENT APPLICATION NUMBER: 09/673,166  
 17 <141> CURRENT FILING DATE: 2001-04-04  
 19 <150> PRIOR APPLICATION NUMBER: PCT/FR99/00792  
 20 <151> PRIOR FILING DATE: 1999-04-06  
 22 <160> NUMBER OF SEQ ID NOS: 276  
 24 <170> SOFTWARE: PatentIn Ver. 2.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 14  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Clostridium tetanus  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: amino acids 830-843 of the tetanus toxin  
 34 <400> SEQUENCE: 1  
 35 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu  
 36 1 5 10  
 39 <210> SEQ ID NO: 2  
 40 <211> LENGTH: 14  
 41 <212> TYPE: PRT  
 42 <213> ORGANISM: Human Papillomavirus (HPV)  
 44 <220> FEATURE:  
 45 <223> OTHER INFORMATION: amino acids 43-57 of HPV E7 protein  
 47 <400> SEQUENCE: 2  
 48 Gly Gln Ala Glu Pro Asp Arg Ala His Asn Ile Val Thr Phe  
 49 1 5 10  
 52 <210> SEQ ID NO: 3  
 53 <211> LENGTH: 28  
 54 <212> TYPE: PRT  
 55 <213> ORGANISM: Artificial Sequence  
 57 <220> FEATURE:  
 58 <221> NAME/KEY: LIPID  
 59 <222> LOCATION: (1)  
 60 <223> OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue  
 62 <400> SEQUENCE: 3

Does Not Comply  
 Corrected Diskette Needed

pp 1-3

(see item 11 on Encl  
 Summary Sheet)

The source of genetic material  
 for the entire  
 Artificial  
 Sequence needs  
 to be  
 explained. 8/19/02

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63 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu  
 64 1 5 10 15  
 66 Ala Ala Ala Ala Ala Gly Ile Gly Ile Leu Thr Val  
 67 20 25

70 &lt;210&gt; SEQ ID NO: 4

71 &lt;211&gt; LENGTH: 28

72 &lt;212&gt; TYPE: PRT

73 &lt;213&gt; ORGANISM: Artificial Sequence

75 &lt;220&gt; FEATURE:

76 &lt;221&gt; NAME/KEY: LIPID

77 &lt;222&gt; LOCATION: (1)

78 &lt;223&gt; OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue

80 &lt;400&gt; SEQUENCE: 4

81 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

82 1 5 10 15

84 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val

85 20 25

88 &lt;210&gt; SEQ ID NO: 5

89 &lt;211&gt; LENGTH: 28

90 &lt;212&gt; TYPE: PRT

91 &lt;213&gt; ORGANISM: Artificial Sequence

93 &lt;220&gt; FEATURE:

94 &lt;221&gt; NAME/KEY: LIPID

95 &lt;222&gt; LOCATION: (1)

96 &lt;223&gt; OTHER INFORMATION: dipalmitoyl-lysyl chain on N-terminal residue

98 &lt;400&gt; SEQUENCE: 5

99 Gly Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

100 1 5 10 15

102 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val

103 20 25

106 &lt;210&gt; SEQ ID NO: 6

107 &lt;211&gt; LENGTH: 28

108 &lt;212&gt; TYPE: PRT

109 &lt;213&gt; ORGANISM: Artificial Sequence

111 &lt;220&gt; FEATURE:

112 &lt;221&gt; NAME/KEY: LIPID

113 &lt;222&gt; LOCATION: (1)

114 &lt;223&gt; OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue

116 &lt;400&gt; SEQUENCE: 6

117 Ser Ser Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu

118 1 5 10 15

120 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val

121 20 25

124 &lt;210&gt; SEQ ID NO: 7

125 &lt;211&gt; LENGTH: 28

126 &lt;212&gt; TYPE: PRT

127 &lt;213&gt; ORGANISM: Artificial Sequence

129 &lt;220&gt; FEATURE:

130 &lt;221&gt; NAME/KEY: LIPID

*entire sequence needs to be explained**same error*

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131 <222> LOCATION: (1)  
 132 <223> OTHER INFORMATION: monopalmitoyl-lysyl chain on N-terminal residue  
 134 <400> SEQUENCE: 7  
 135 Gly Arg Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu  
 136 1 5 10 15  
 138 Arg Gly Arg Ala Ala Gly Ile Gly Ile Leu Thr Val  
 139 20 25  
 142 <210> SEQ ID NO: 8  
 143 <211> LENGTH: 10  
 144 <212> TYPE: PRT  
 145 <213> ORGANISM: Artificial Sequence  
 147 <220> FEATURE:  
 148 <223> OTHER INFORMATION: A hydrazine is bound between the N-terminal lysine  
 149 and isoleucine at position 2  
 151 <400> SEQUENCE: 8  
 152 Lys Ile Leu Lys Glu Pro Val His Gly Val  
 153 1 5 10  
 156 <210> SEQ ID NO: 9  
 157 <211> LENGTH: 15  
 158 <212> TYPE: PRT  
 159 <213> ORGANISM: Artificial Sequence  
 161 <220> FEATURE:  
 162 <223> OTHER INFORMATION: aldehyde group bound to N- terminal residue  
 164 <220> FEATURE:  
 165 <221> NAME/KEY: LIPID  
 166 <222> LOCATION: (15)  
 167 <223> OTHER INFORMATION: palmitoyl chain on C-terminal lysine residue  
 169 <400> SEQUENCE: 9  
 170 Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Lys  
 171 1 5 10 15  
 174 <210> SEQ ID NO: 10  
 175 <211> LENGTH: 9  
 176 <212> TYPE: PRT  
 177 <213> ORGANISM: Homo sapiens  
 179 <220> FEATURE:  
 180 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic  
 181 myeloid leukemia translocation)  
 183 <400> SEQUENCE: 10  
 184 Glu Asp Ala Glu Leu Asn Pro Arg Phe  
 185 1 5  
 188 <210> SEQ ID NO: 11  
 189 <211> LENGTH: 9  
 190 <212> TYPE: PRT  
 191 <213> ORGANISM: Homo sapiens  
 193 <220> FEATURE:  
 194 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic  
 195 myeloid leukemia translocation)  
 197 <400> SEQUENCE: 11  
 198 Ser Glu Leu Asp Leu Glu Lys Gly Leu

*Please correct this error  
in subsequent sequences*

RAW SEQUENCE LISTING  
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199      1              5
202 <210> SEQ ID NO: 12
203 <211> LENGTH: 9
204 <212> TYPE: PRT
205 <213> ORGANISM: Homo sapiens
207 <220> FEATURE:
208 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
209      myeloid leukemia translocation)
211 <400> SEQUENCE: 12
212 Asp Glu Leu Glu Ala Val Pro Asn Ile
213      1              5
216 <210> SEQ ID NO: 13
217 <211> LENGTH: 9
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <220> FEATURE:
222 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
223      myeloid leukemia translocation)
225 <400> SEQUENCE: 13
226 Lys Glu Asp Ala Leu Gln Arg Pro Val
227      1              5
230 <210> SEQ ID NO: 14
231 <211> LENGTH: 9
232 <212> TYPE: PRT
233 <213> ORGANISM: Homo sapiens
235 <220> FEATURE:
236 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
237      myeloid leukemia translocation)
239 <400> SEQUENCE: 14
240 Glu Asp Ala Leu Gln Arg Pro Val Ala
241      1              5
244 <210> SEQ ID NO: 15
245 <211> LENGTH: 9
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
249 <220> FEATURE:
250 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
251      myeloid leukemia translocation)
253 <400> SEQUENCE: 15
254 Gly Glu Lys Leu Arg Val Leu Gly Tyr
255      1              5
258 <210> SEQ ID NO: 16
259 <211> LENGTH: 9
260 <212> TYPE: PRT
261 <213> ORGANISM: Homo sapiens
263 <220> FEATURE:
264 <223> OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic
265      myeloid leukemia translocation)
267 <400> SEQUENCE: 16

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## RAW SEQUENCE LISTING

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268 Glu Asp Thr Met Glu Val Glu Glu Phe

269 1 5

272 &lt;210&gt; SEQ ID NO: 17

273 &lt;211&gt; LENGTH: 9

274 &lt;212&gt; TYPE: PRT

275 &lt;213&gt; ORGANISM: Homo sapiens

277 &lt;220&gt; FEATURE:

278 &lt;223&gt; OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic

279 myeloid leukemia translocation)

281 &lt;400&gt; SEQUENCE: 17

282 Met Glu Tyr Leu Glu Lys Lys Asn Phe

283 1 5

286 &lt;210&gt; SEQ ID NO: 18

287 &lt;211&gt; LENGTH: 9

288 &lt;212&gt; TYPE: PRT

289 &lt;213&gt; ORGANISM: Homo sapiens

291 &lt;220&gt; FEATURE:

292 &lt;223&gt; OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic

293 myeloid leukemia translocation)

295 &lt;400&gt; SEQUENCE: 18

296 Asn Glu Glu Ala Ala Asp Glu Val Phe

297 1 5

300 &lt;210&gt; SEQ ID NO: 19

301 &lt;211&gt; LENGTH: 9

302 &lt;212&gt; TYPE: PRT

303 &lt;213&gt; ORGANISM: Homo sapiens

305 &lt;220&gt; FEATURE:

306 &lt;223&gt; OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic

307 myeloid leukemia translocation)

309 &lt;400&gt; SEQUENCE: 19

310 Val Asn Gln Glu Arg Phe Arg Met Ile

311 1 5

314 &lt;210&gt; SEQ ID NO: 20

315 &lt;211&gt; LENGTH: 9

316 &lt;212&gt; TYPE: PRT

317 &lt;213&gt; ORGANISM: Homo sapiens

319 &lt;220&gt; FEATURE:

320 &lt;223&gt; OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic

321 myeloid leukemia translocation)

323 &lt;400&gt; SEQUENCE: 20

324 Leu Phe Gln Lys Leu Ala Ser Gln Leu

325 1 5

328 &lt;210&gt; SEQ ID NO: 21

329 &lt;211&gt; LENGTH: 9

330 &lt;212&gt; TYPE: PRT

331 &lt;213&gt; ORGANISM: Homo sapiens

333 &lt;220&gt; FEATURE:

334 &lt;223&gt; OTHER INFORMATION: epitope from BCR-ABL fusion protein (chronic

335 myeloid leukemia translocation)

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